



FIG. 1A

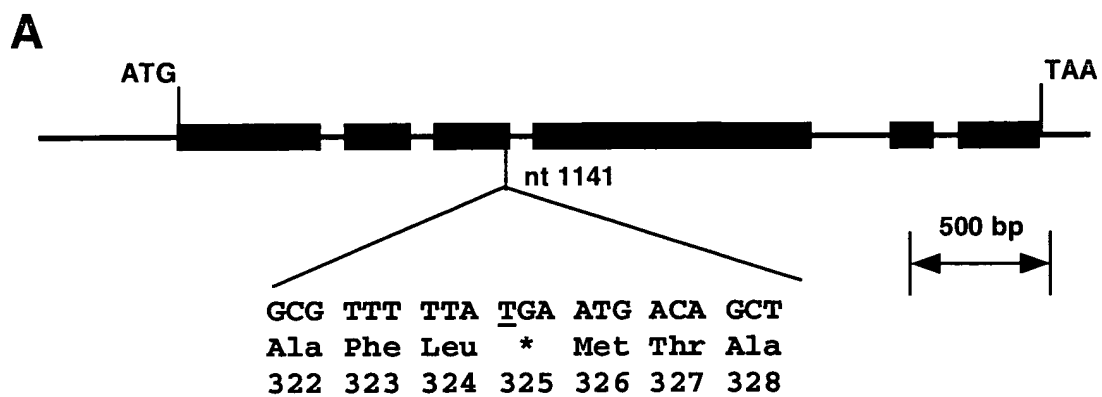


FIG. 1B

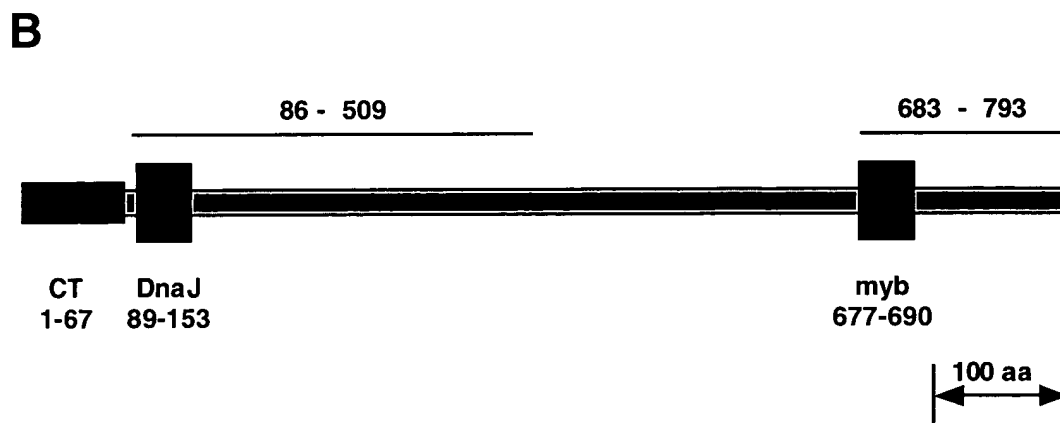


FIG. 2

Q9SAG8/55-115	DPYKTLKURPD	SSSEYE	VKKAFRLAKKYHPDVCRGSN	CGV	QFOTNEAYDVLKQ	IKQOME
P93499/67-134	SLYDILGIPAG	ASSQE	IKAAVRLARVCHPDVAID	RKNSSADE	FMKTHAAYST	SPP-DKRAHYD-RSL-
O48828/68-135	SLYEILETPVG	STSQE	IKSAVRLARICHPDVARN	RDNSSADD	FMKTHAAYCTLS	DP-EXRAVYD-RRT-
DNJL_MYCPN/2-64	TYDILLELPQT	ATLOE	IKTAYKRLAKRYHPDINKQ	GADT	FVKTNNAAYVLS	ST-TQKAEYD-AML-
DNJL_MYCGE/2-64	NLYDILLELPTT	ASIKE	IKIAVYKRLAKRYHPDVNKL	GSQT	FVEINNAYSILS	DP-NQKEKYD-SML-
Q9SDN0/66-133	SYDILLGVTES	VTLPE	IKQAYKOLARKYHPDVSPPD	RVEEYDTR	FIRQOEAYETLSD	DP-RRRVLYD-RDL-
Q9VXT2/31-99	NCYDVLGVTR	SSKSE	IGKAYRQLARRYHPDLHRGA	EAKAAAEQ	FKLVATAYEILRE	DP-ESRTDYD-YML-
Q17433/36-105	NCYDYLEANREE	FDKQK	LAKAYRQLARKYHPDVKNK	EEKLLAEER	FRVITATAYETL	KDD-EAKTYD-YYL-
Q9SH08/76-147	SPYDTLELDRN	AEEEQ	IKVAVRRLAKFYHPDVVDKGG	TLEEGETAER	FIKIQAAAYEL	MDS-EKKVQYD-MDN-
O94657/6-73	KLYDILEVHFE	ASAE	IKKSYKRLALLHHPDZAPIH	EKEEAAER	FRGVQOEAYDIL	KDP-ESREMYD-MYG-
*maize	DFYKULCAEP	HFLGD	GIRRAFESR-IAKPPQYGY	TEALAGRQ	MLQIAHDTLTNQ	SSRTEYD-RALS
*rice/97-162	DFYKULGAEP	HFLGD	GIRRAFEAR-IAKPPQYGY	TDALVGRQ	MLQIAHDTLMNQ	NSRTQYD-RALS
*potato/109-174	DFYRVLGAEA	HFLGD	GIRRCYDAR-ITKPPQYGY	QEAALIGRQ	ILQAAACETLAD	S-TSRREYN-QGLA
*Mtrunc/	DIYKULGAET	HFLGD	GIRRAYEAK-FSKPPQYAF	S-NEALISRRQ	ILQAAACETLAD	P-ASRREYN-QSLV
*Athal/89-154	DFYQVLCQAOT	HFLTD	GIRRAFEAR-VSKPPQFG	S-DDALISRRQ	ILQAAACETL	SNP-RSRREYN-EGLL
*Pm_MED4/6-71	DHFRILGVSP	SATSE	EILRAFQLR-LDKTPDEG	FT-YEVLTORSE	LIRLTADLITDP	-DSRRDYE-NLLL
*Pm_MIT9313/11-76	DHFRILGVSP	SADSE	AILRALELR-LDRCPPDQ	GFT-HEVLIQRAE	LIRLSADLITDP	-PRQAYE-TALL
*Secc_WH8102/6-71	DHFRILGVSP	SADPA	SILRRLQTR-SDSPDDG	FT-HEGLLQRA	LILHRSADLITDP	-SERADME-AALL
*Syn_PCC6803/6-71	DFYRILGIPP	QSGGE	TIEQAYQDR-LLQLPRR	EPS-DAAVTLRQ	LIAIAYETLRDP	-EKRQAYD-QEWM
*Nostoc/6-71	DYRILGLPL	ASSEE	QLRQAYSDR-IVQLPRR	EYS-QAAISSRQ	LIEEAYVLS	DP-KQSTYD-QLYL
*Anabena/16-81	DYRILGLPL	ASDE	QLRQAYSDR-IVQLPRR	EYS-QAAISSRQ	LIEEAYVLS	DP-KQSTYD-QLYL
Q9U6V7/17-82	DYNALLGCDE	NSTVE	QITAEYKILALQYHPD	KNDG-EKEAEMFQ	LIEEAYVLS	DP-KERSSYD-QLYL
Q9TVP3/17-82	DFYGLLHCDE	NSSPE	QITAEYKILALQYHPD	KNSG-DKEAEAKFQ	QLKEAKETL	CDP-EXRAIYD-KWR-
Q9R022/14-79	DYNALLGCDE	LSVE	QLAEFKILALQYHPD	KNSG-DKEAEAKFQ	QLKEAKETL	CDP-EXRAIYD-KWR-
Q9VN28/708-772	DANSTILGVPP	DSSQE	QIRKHYKKTAVLVHPD	KNK-QAGAEAEFK	VLQRAFEL	LIGEP-ENRLIYD-QSI-
O97211/9-72	ELAYQMLELDA	QCTTA	EISQYRRLALRYHPD	RNAG-ATVEQFQ	RUEEAHRL	SDL-RQRLIYD-TVG-
O13601/12-78	DYNTILGAES	TSSYV	EIRQYKILVLRYPD	RNPGRGAEVLPQFQ	LQKAHEV	LKDP-KIRELFD-QRR-
O94566/12-78	DYNALLKLQK	NATFQ	QIRKQYLELALQYHPD	RNPGRGAEVLPQFQ	LQKAHEV	LSDA-TKRLIYD-QLF-
Q9UUG3/2-69	NHNSVNLKDGK	TYTDD	EIKRAYRKALLLHFPD	KCK-EKPSVWYTIDQ	VKEAYQVLS	SE-KIROQYQ-IKQ-

FIG. 3A

Anabena	6	QGVYVR	PLDYRILGLPLA	SEQLRQAVSR	IVQLPREYSQAATA	SRKQLTEEA	VVVLSDPK	SSVSDQLYL	AHAYDPD	NAATT	TKVA	VENRGDSN	
Nostoc	1	MRPE	DYRILGLPLA	SEQLRQAVSR	IVQLPREYSQAATA	SRKQLTEEA	VVVLSDPK	SSVSDQLYL	AHAYDPD	NAATA	VAQENR	TST	
Pm_MED4	1	MELP	DYRILGLPLA	SEQLRQAVSR	IVQLPREYSQAATA	SRKQLTEEA	VVVLSDPK	SSVSDQLYL	AHAYDPD	NAATA	VAQENR	TST	
Pm_MT9313	1	MAAQL	VDLPLDHYRIL	GLVSPSADSE	AILRALER	DRCPDGETHE	VILQRAEL	RLISADLL	TDPPRQAV	ETALLE	LSRD	---	
Syn_PCC6803	1	---	MPLD	YRILGLIP	PPQSGTE	IQADRLQL	PREESDAAV	IRNQLHAT	YETLRD	PEKQAV	QEWNG	---	
Scc_PCC7002	1	---	MPLD	YRILGLIP	PPQSGTE	IQADRLQL	PREESDAAV	IRNQLHAT	YETLRD	PEKQAV	QEWNG	---	
Scc_WH8102	5	GDLW	THDPLDHYRIL	GLVSPSADSE	AILRALER	DRCPDGETHE	VILQRAEL	RLISADLL	TDPPRQAV	ETALLE	LSRD	---	
rice	87	AAERS	STPQVDFM	KVGLGAE	PHFLG	DGIRRA	FAEATK	APPOVGY	STDALVGR	OMLOI	AHDTLM	QNSTQYDRALS	ENR
Athal	79	RPER	HVPI										

FIG. 3B

	410	420	430	440	450	460	470	480	490	500
Anabena	294 VAEGHKLFDGSKK--RPSAVATYLVAVTASIAAGFTQCPALITREAKQILMRIKKR---QDVHLEQSLSCLALTECOTEEATRVLLEL									
Nostoc	284 VAEGHKLFEAQSK--RSSAVATYLAVVLTIAARGFAQCIPALITROARQMVLVKRK---QDVHLEQSLSCLALTECOTEEATRVLLEL									
Pm_MED4	245 VOIQIDFLFLELQK--RGSSEAGELAFISLTIAIGFARKPKAKTFEARKILLKKLNLSG---LDSPMLIGSLCLDLEADVEQSSARFELS									
Pm_MT9313	257 VQEIVDFLFRWQQ--AGSADAGEFLGLIALAAGFSRRKPERVQEARQHLLERQLDQG---CDPLFMIGSLCLDLEGDVGRAQERFLR									
Syt_PCC6803	253 VAEQNALFLPESQ--RPSLVASNLAVHSMAEGVKEDPMATVEAKSLIIQIENC---QDLALEKVICBELLTCOTEVVLAAIDQ									
Scc_PCC7002	280 VQEQLDLFFVAESK--RPSAAAAYLAVVALLAAGFSOMKPDLYVCAQTLLKRILKKR---QDVFLFEQSICALITEGPSEANQLLEQ									
Scc_WH8102	262 VQEIVDFLFRGWFA--EGSIRAGCLAVFALAAGAYSRRKPETFEQAEREQLQRVLVASD---LDPMPLLRGSLCLDLEGNVAEASHFSA									
rice	327 SIEQMDFFSKTPNSIPPWEFIINVALAHVAQAIISSKPOFMMADDLFEQLQXFNIG----SHYAYDN-----EMDLALERAFCSLLGVDSVKCRMWLGI									
Athal	328 AAEGVDLFLVATPSNIPAESFEVMEVALVAQAQFIGKHPIHQADKQFOQLQQAQVMAMEIPAMLYDYTRNNWEIDFGLERGLCALTEGDKVDECRMWLGL									
potato	197									

[illegible][illegible]

FIG. 3C

[illegible]

Human_Dynam-in-1	1	-----MGNRQMEDLIPLVNRLODAPS-----AIGQNADLDLPQIAVVGQSAGKESVLENFVGR
Yeast_Dnmlp	1	-----MAS--LEDLIPTVNRKLDVMY-----DSGIDT-LDLA-ILAVGQS88GKESILNLTIVGR
ARC5	1	MAEVSAKSVTVENAEEDDAIIEERWSLYEYNELHALAOELTPPEAPVAVLHVGQOTDGSALVIALMGF
Human_Dynam-in-1	64	VEEREDVQOLVNAIT-----EYAEPELHCKOKKET
Yeast_Dnmlp	61	VEERPLVQENNISPNISPLIEEDDNSVNPHEVTKISGPEAGTRPLEYRGKERNHAEDEWGESEHIPPGRREY
ARC5	81	KERRELTTHMKYDQPCPP-----LCHLGSDDDDPSVSLPK
Human_Dynam-in-1	102	EARTDEVGT-NKGISPVPEINRKYSPHVLMEGLVDLEGTKVVGQD--PPDIEFQIRDMEMQFVTKBNC
Yeast_Dnmlp	141	ENETATIAK-DKGISKEPHNRKVPSPHVMGLVGLGKTKVFGEO--PPDIEKQKKNELLDYIATPNC
ARC5	125	EAKNMEDEQBPCSEPPSAKEHIVKQYKPCPELTIDTGLIAPAPQKLNALQVQARAVEALVRKMQHKE
Human_Dynam-in-1	179	QDLANSDAIKVAKHVEEQGQKMGVIAKUDMDDEGTDAADVLENKLLERRGYIGVNVRSQKDDIGKEDIT
Yeast_Dnmlp	218	VLNVSESILKARAVDQGRKRGVIRKDDGMDSGENALDILSGKMYELKLGFGVGVNRSQDIQLNETVE
ARC5	205	GDWSIATTRVLMQVDELSRUVVSKEDTKIPQFSCSDVEVFLSEP-----ASALDSLLGDSPPP
Human_Dynam-in-1	259	FLSHPSYRHEADRMGTPYIQKVINOQLTNEHRTDTPGLRNKLOQLLSBKVBHBYKNRPDDPARKTKAL
Yeast_Dnmlp	298	FRKEHVMRTI-STKCGTRYEAKLNQTLSSHIRDKLPDITKLNELISQTEQELARYGCVGATTNESRASLV
ARC5	278	YGQDSYVKNSEDPKQAVSIREMEDIASLEKELGRLTKQESHRIGISKRLRFLFEBLLYKRYKESVPLIPI
Human_Dynam-in-1	339	DEERAKSCGQDQIDTYEESC-GARINRLEHERPPPELVMEPPDERKELRREISYAIKNIHQIRIGITPDMA
Yeast_Dnmlp	378	NEISSIDGSSDINTRELCO-GARLYIYNVNVGNSEKSIDPTSNLSVLDVRIARNSTGPRPTLEVEBELA
ARC5	358	RKLDVSKELSSIDBAKNERGRTPHDLGLTKLSLLKGTVPAPDPKPGETLQDERTQCGAPV@TDGLQPG
Human_Dynam-in-1	418	KKTRHPCLKQVDMOISEEL-----STVRQC-TKKLQVPRLEEMERIYTHIREREGRTKEQVM
Yeast_Dnmlp	457	KLLLEPSQRCVRLVBEELM-----KICHKCGSAGEARPKKSMLEIVISBLRERLQPTRSYVE
ARC5	438	RLYGGAQYHRAMAEERELVGAIKCPPITREIEVNA@VEDHEDGTNYSRTACVIAVAKARETFEFLHQLG
Human_Dynam-in-1	486	ENTNHEDELOFANAQQRSNQMNRRKTSQDQBELVIRKGMITINNIGIMKQGSSEYWPVLTAEMLSWYKDD
Yeast_Dnmlp	526	ENTNHEPNEL--SATEAMDDINKTRKRNQ--LLESKESQENGOINGING-----TSSISNIDQD
ARC5	518	ULPISVYLLQKBGEYLSQHEVPLEEVASAFNPFVSTESKSCRDKCHEDTASTR-----YVTW@LHNKN
Human_Dynam-in-1	566	SVDNKLRDVERGFMSSKHIFALPN-EEQRNVYKDYRQLELACETQEEVDSWKASELRAGVYPERVGDKEK
Yeast_Dnmlp	593	DGIDAHSKQTKDKLN--YFEGKDK-KGQVPDASDEKRSINQD-----GNIBDERNLQSDPSLGDIDD
ARC5	591	SPGCTEHNITSGNATGFSLPQDALGGTIDTRSRSDVKLSHEASNIDSGSSIQTTEMRLADLDSLWNRL
Human_Dynam-in-1	645	DSPMHSMDPQLERQVETIRNLVDSYMAIVNKTMRDLMPEITIMHLMNTRKTFPSSELANEYSCGQNTER
Yeast_Dnmlp	661	-----PETERBELSCPRKTRIVSVPDIREMIEDQVPRAYMCLIVNYCKDSVQNRRLVTKRYKETLPREEL
ARC5	668	-----IVYALVQQEPQGEREYELASAEELKFNCFLEMPVDEKPEALLREBEENAPEDDUDSIFDITNER
Human_Dynam-in-1	725	RDEMLRMVHALKEALSTIGNINTITVSTPMFPPVDSDSWLQVQSVAPAGRRSPTSSPTPQRRAPAVPPARPGS
Yeast_Dnmlp	736	RELCKVKS@GVYKKAATLISNII-----
ARC5	740	TEBELRVRK@KEKPRV@NNEKLN@HEPAQN-----LKAPS@QH-----
Human_Dynam-in-1	805	AGSALGGAPPVPSRPGASDPDPGPPPPQVPSRPNRAPPGVPSRSGQASPSRPPPPDL
Yeast_Dnmlp		-----
ARC5		-----

FIG. 4